

1/4

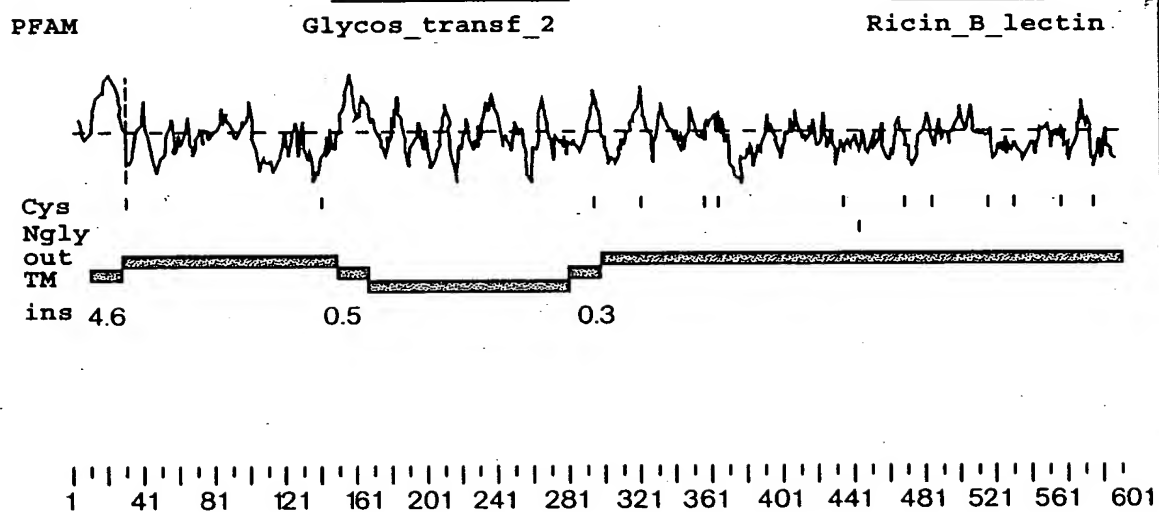


Fig. 1

Glycos_transf_2: domain 1 of 1, from 154 to 336: score 55.7, E = 1e-12
 *->sivIptYNeeadyLeelleSvlaqs.tledieiivvDDgSetDetve
 s+v + Ne+++ +++ ++Sv + + + e+i vDD+S + e++
 47174 154 SVVFIFVNEALSVILRSVHSVNHtpSQLLKEVILVDDNSDNVELKF 200
 iaedylderikeenpriiivirleensqGpaaArnkgirratGdsdyIlf
 ++ y+ ++ +p + ++r++++ G +Ar +g ++at ++ f
 47174 201 NLDQYV---NKRYPGLVKIVRNSRRE-GLIRARLQGWKAATAP--VVGf 243
 LDaDdiftpdkleklidyaeatdaavvlgaida.....yeyaegesnlr
 +Da+++f ++ e+++++++ +++ +vl+aid + +++e +++ + ++
 47174 244 FDAHVEFNTGWAEPALSRIREDRRRIVLPAIDNikystFEVQQYANA-AH 292
 iaradterslfagllrktgrltgglelsfeigsnaiyrreafeelf<-*
 ++++ ++ ++ +++ +r g+ ++ +++++ + ++ +++e+f
 47174 293 GYNWGLWCMYIIPPQDWLDR--GDESAPIRTPAMIGCSFVVDREYF 336

Fig. 2

Alignments of top-scoring domains:

```
ricin_3: domain 1 of 1, from 465 to 595: score 32.5, E =9.8e-06
      *>rgyfliiggntglCLdvngnsesksdGnpvglwdChgggnQlWkltY
      +g ++ + ++ CLd +++++ + +l++Chg ++Ql +++
47174  465  YGEVRNSK-ASAYCLDQGAEDGD-----RAILYPCHGMSSQLVRYS- 504
      nesdgairi.....nsdlCLtvng...tvtylsCdgtckgndnQk.
      dg + ++ +++ + +CL +g+++ tl++C++ + + Q+
47174  505  --ADGLQLGplgstafIPDSKCLVDDGtgrMPTLKKCEDV--ARPTQRl 550
      WevndkgcirnpknskkgvdsglcLdvkdgn.....kvqlwtcngsdap
      W + ++g i+++ +g cL+v +++ + + +++ c+g
47174  551  WDFTQSGPIVSR-----ATGRCLEVEMSKdanfglRLVVQRCSG----- 589
      nQkWife<-*
      QkW ++
47174  590  -QKWMIR 595
```

Fig. 3

4/4

>2308 p99.2 (23) PAGT(3) // N-ACETYL GALACTOSAMINYLTRANSFERASE TRANSFERASE
POLYPEPTIDE ACETYL GALACTOSAMINYLTRANSFERASE UDP-GALNAC:POLYPEPTIDE
GLYCOSYLTRANSFERASE PROTEIN-UDP PROTEIN-UDP N-
LENGTH = 172

Score = 423 (154.0 bits), Expect = 4.7e-40, P = 4.7e-40
Identities = 77/151 (50%), Positives = 104/151 (68%)

Query: 312 RGDESAPIRTPAMIGCSFVVDREYFGDIGLLDPGMEVYGGENVELGMRVWQC GGSMEVLP 371
R D + PIR+P M G F +++EYF ++G DPGM+++GGEN+EL RVWQCGG +E++P
Sbjct: 14 RKDPTDPIRSPTMAGGLFAINKEYFEELGTYDPGMDIWGGENLELSFRVWQCGRLEIVP 73

Query: 372 CS RVAHIERTRKPYNNIDYYAK----RNALRAAEVWMDDFKSHVYMAWNIPMSNPGVDF 427
CS V H+ R R PY K RN +R AEVWMDD+K + Y + P + DF
Sbjct: 74 CSHVGHVFRKRSPYTFPGKSGKDVISRNTVRVAEVWMDDYKEYFYK--HNPQARKVRDF 131

Query: 428 GDVSERLALRQRLKCRSFKWYLENVYPEMRV 458
GD+SER LR++L+C+SFKWYLENVYP++ V
Sbjct: 132 GDISERKELREKLQCKSFKWYLENVYPDLYV 162

Fig. 4